RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/041,859

DATE: 01/27/2002
TIME: 15:30:42

Input Set : A:\087102us.app
Output Set: N:\CRF3\01272002\J041859.raw

PS


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  3 <110> APPLICANT: HUANG, QIHONG
  4       REED, JOHN C.
  5       DEVERAUX, QUINN L.
  6       MAEDA, SUSUMU
  8 <120> TITLE OF INVENTION: INHIBITOR OF APOPTOSIS PROTEINS AND NUCLEIC ACIDS AND
  9       METHODS FOR MAKING AND USING THEM
 11 <130> FILE REFERENCE: 087102/027 2537
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/041,859
C--> 14 <141> CURRENT FILING DATE: 2002-01-07
 16 <150> PRIOR APPLICATION NUMBER: 60/260,478
 17 <151> PRIOR FILING DATE: 2001-01-08
 19 <160> NUMBER OF SEQ ID NOS: 25
 21 <170> SOFTWARE: PatentIn Ver. 2.1
 23 <210> SEQ ID NO: 1
 24 <211> LENGTH: 3773
 25 <212> TYPE: DNA
 26 <213> ORGANISM: Bombyx mori
 28 <220> FEATURE:
 29 <221> NAME/KEY: CDS
 30 <222> LOCATION: (2733)..(3770)
 32 <400> SEQUENCE: 1
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 37 ttcttgcaag acgagtgtca gtgattaaac aaaaacataa gaatagacgt tttatgcgtt 180
 39 actaaaaaaa aggaaaaata taccaatgga gttgacgaaa gttgctaaaa atggagctgc 240
 41 cgccacgttg gtgatgttaa aaaatgcgcg ggatgcaaaa atgcgacctt tcattggtcc 300
 43 gctcatgtta tcctcgtgtg agtcttcaac gacatccaca ctcccgtcac cttcgtcgtc 360
 45 agctgataaa acggataatc acgacacatt caacttcctt cctgatatgc ccgacatgcg 420
 47 tcgtgaagag gaacgtctga aaacatttga tcagtggccc gttacgtttt tgacgccgga 480
 49 acaattggcc cgcaacggat tctactacct cggtcgcggc gacgaagtgt gctgtgcttt 540
 51 ctgtaaggta gaaattatga ggtgggtcga aggcgacgat cctgccgccg atcatcggag 600
 53 atgggcgccc cagtgtccct ttgtacgaaa acaaatgtat gccaacgctg ggggagaggc 660
 55 gaccgctgtc ggtagagacg aatgtggggc cagtgcggcc acgcagcctc cccgcatgcc 720
 57 cggccccgtg cacgcgcggt actccaccga ggccgcgcgg ctcgccacct tcaaggactg 780
 59 gccgagacgt atgcgccaaa aacccgagga actggcagag gccggattct tctatacagg 840
 61 ccaaggtgac aaaacgaaat gcttctattg cgacggaggg ctaaaagatt gggaaagcga 900
 63 tgacgttccg tgggaacagc acgccagatg gttcgaccgc tgcgcgtacg tgcaattggt 960
 65 gaaaggacgt gactacattc agaaggtgaa gtcggaggcc actgcgatat ctgctagcga 1020
 67 agaagaacag gccgccacca atgattcgac taagaacgtc gcccaagagg gcgagaaaca 1080
 69 tttggatgac tctaaaatat gtaaaatatg ttattccgag gagcgtaacg tgtgcttcgt 1140
 71 gccgtgcggc cacgtggtgg cgtgcgccaa gtgcgcgctg tcgacggaca agtgcccgat 1200
 73 gtgtcgcagg acgttcacga atgcggtgcg gctctacttc tcgtgaaagg accctcctcg 1260
 75 cgagctgtat actaatcact tcaccgggcg gccctggagc gtgctgaaac caccccttcga 1320
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77 acgaaaccgc gtatcctgtg atttttacat taaataaatt tacaaattga tagcggtggg 1380
79 gcaatgtata ggaactcgtc agaactcgcg agttgacgtg caggaaggag ttagtgattt 1440
81 gtaaacttgt aaactgatgt tgaaatgatt ttatttatta tttaaaattc taatgacaaa 1500
83 gtgtaagtaa ataaatgtac atattatttt agattatcag tttgtcccac cgacaaaagt 1560
85 gaaatgtaca taggtgtttt catatcactt caacagtcga agaccttctt tttgaattta 1620
87 aggatatata tttatacata taaattaaaa ttttaacgag acatcaatat aaatggttta 1680
89 acaacttatt tatacactga aatcaagtga agtgtaacat ggtctgaaga atgttttact 1740
91 gatttcactt cccctgttga agtgataaaa ttctaatgta aatccagagt ttaaatgtcg 1800
93 tcataattaa tataagaaac aagttttacg cttcttttgc ttgaaaaatc ttataattga 1860
95 ttcaggaatt atttaatgtg actatatttt gttcctgtaa ataacataat atatactatt 1920
97 tattgattaa ttctgacata atttatggca attccgtaag atacaatcca atacttattt 1980
99 catgtaactc acttcaaaat agttgaatgt gtggtgtgat tataatgtta aatgtctaaa 2040
101 tttataataa attgagcaaa gttgcattta atgtatgaat actaattatt gttttaacaa 2100
103 aacatttaag tataatctgc tctgtgattt taatgtatca agaaataacc ccaacacctt 2160
105 aattgaagtt tttacattgt tgctgataaa aaaaatcata tcaattacat ttacaagtca 2220
107 attttaattg ttcagaaacc aaacacaatt ttgttagtga ctcctgcttt acgaagtagt 2280
109 atgacaaacc agtgtttcgt tgattgcatt aatttagttg taaccaatat ttacactcaa 2340
111 cattttaaga tgtcattgag gaattctgta taaaaaatgg gaatttattt attggtgtat 2400
113 aatacaatcc cgcacaagcc atttgcaagt ttctacacaa ctaaaacgta ttgtatccat 2460
115 tatctatacg tcatatcatt aatatatact tgctttagca aacatatatt cacgaataac 2520
117 ttcacaatat atttttgtaa atcaacatat taatggtaat taacgaatcg cacggtacaa 2580
119 atagtgataa ctgctgagtg cactaaatag taagagaatt tatttaaaca gtcaaatttt 2640
121 gtttcataag tagttatttc atactgttga atgttattca ttaaaacaaa tgttaaagca 2700
123 aaaaaaaaaa aaaaaagtcg tgactgggaa aa atg gag ttg acg aaa gtt gct   2753
124                                    Met Glu Leu Thr Lys Val Ala
125                                      1               5
127 aaa aat gga gct gcc gcc acg ttg gtg atg tta aaa aat gcg cgg gat   2801
128 Lys Asn Gly Ala Ala Ala Thr Leu Val Met Leu Lys Asn Ala Arg Asp
129          10                  15                  20
131 gca aaa atg cga cct ttc att ggt ccg ctc atg tta tcc tcg tgt gag   2849
132 Ala Lys Met Arg Pro Phe Ile Gly Pro Leu Met Leu Ser Ser Cys Glu
133      25                  30                  35
135 tct tca acg aca tcc aca ctc ccg tca cct tcg tcg tca gct gat aaa   2897
136 Ser Ser Thr Thr Ser Thr Leu Pro Ser Pro Ser Ser Ser Ala Asp Lys
137  40                  45                  50                  55
139 acg gat aat cac gac aca ttc aac ttc ctt cct gat atg ccc gac atg   2945
140 Thr Asp Asn His Asp Thr Phe Asn Phe Leu Pro Asp Met Pro Asp Met
141                  60                  65                  70
143 cgt cgt gaa gag gaa cgt ctg aaa aca ttt gat cag tgg ccc gtt acg   2993
144 Arg Arg Glu Glu Glu Arg Leu Lys Thr Phe Asp Gln Trp Pro Val Thr
145              75                  80                  85
147 ttt ttg acg ccg gaa caa ttg gcc cgc aac gga ttc tac tac ctc ggt   3041
148 Phe Leu Thr Pro Glu Gln Leu Ala Arg Asn Gly Phe Tyr Tyr Leu Gly
149          90                  95                  100
151 cgc ggc gac gaa gtg tgc tgt gct ttc tgt aag gta gaa att atg agg   3089
152 Arg Gly Asp Glu Val Cys Cys Ala Phe Cys Lys Val Glu Ile Met Arg
153     105                 110                 115
155 tgg gtc gaa ggc gac gat cct gcc gcc gat cat cgg aga tgg gcg ccc   3137
156 Trp Val Glu Gly Asp Asp Pro Ala Ala Asp His Arg Arg Trp Ala Pro
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PATENT APPLICATION: US/10/041,859 TIME: 15:30:42

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157 120                 125                 130                 135
159 cag tgt ccc ttt gta cga aaa caa atg tat gcc aac gct ggg gga gag   3185
160 Gln Cys Pro Phe Val Arg Lys Gln Met Tyr Ala Asn Ala Gly Gly Glu
161             140                 145                 150
163 gcg acc gct gtc ggt aga gac gaa tgt ggg gcc agt gcg gcc acg cag   3233
164 Ala Thr Ala Val Gly Arg Asp Glu Cys Gly Ala Ser Ala Ala Thr Gln
165         155                 160                 165
167 cct ccc cgc atg ccc ggc ccc gtg cac gcg cgg tac tcc acc gag gcc   3281
168 Pro Pro Arg Met Pro Gly Pro Val His Ala Arg Tyr Ser Thr Glu Ala
169     170                 175                 180
171 gcg cgg ctc gcc acc ttc aag gac tgg ccg aga cgt atg cgc caa aaa   3329
172 Ala Arg Leu Ala Thr Phe Lys Asp Trp Pro Arg Arg Met Arg Gln Lys
173 185                 190                 195
175 ccc gag gaa ctg gca gag gcc gga ttc ttc tat aca ggc caa ggt gac   3377
176 Pro Glu Glu Leu Ala Glu Ala Gly Phe Phe Tyr Thr Gly Gln Gly Asp
177 200                 205                 210                 215
179 aaa acg aaa tgc ttc tat tgc gac gga ggg cta aaa gat tgg gaa agc   3425
180 Lys Thr Lys Cys Phe Tyr Cys Asp Gly Gly Leu Lys Asp Trp Glu Ser
181             220                 225                 230
183 gat gac gtt ccg tgg gaa cag cac gcc aga tgg ttc gac cgc tgc gcg   3473
184 Asp Asp Val Pro Trp Glu Gln His Ala Arg Trp Phe Asp Arg Cys Ala
185         235                 240                 245
187 tac gtg caa ttg gtg aaa gga cgt gac tac att cag aag gtg aag tcg   3521
188 Tyr Val Gln Leu Val Lys Gly Arg Asp Tyr Ile Gln Lys Val Lys Ser
189     250                 255                 260
191 gag gcc act gcg ata tct gct agc gaa gaa gaa cag gcc gcc acc aat   3569
192 Glu Ala Thr Ala Ile Ser Ala Ser Glu Glu Glu Gln Ala Ala Thr Asn
193 265                 270                 275
195 gat tcg act aag aac gtc gcc caa gag ggc gag aaa cat ttg gat gac   3617
196 Asp Ser Thr Lys Asn Val Ala Gln Glu Gly Glu Lys His Leu Asp Asp
197 280                 285                 290                 295
199 tct aaa ata tgt aaa ata tgt tat tcc gag gag cgt aac gtg tgc ttc   3665
200 Ser Lys Ile Cys Lys Ile Cys Tyr Ser Glu Glu Arg Asn Val Cys Phe
201             300                 305                 310
203 gtg ccg tgc ggc cac gtg gtg gcg tgc gcc aag tgc gcg ctg tcg acg   3713
204 Val Pro Cys Gly His Val Val Ala Cys Ala Lys Cys Ala Leu Ser Thr
205         315                 320                 325
207 gac aag tgc ccg atg tgt cgc agg acg ttc acg aat gcg gtg cgg ctc   3761
208 Asp Lys Cys Pro Met Cys Arg Arg Thr Phe Thr Asn Ala Val Arg Leu
209     330                 335                 340
211 tac ttc tcg tga                                               3773
212 Tyr Phe Ser
213 345
216 <210> SEQ ID NO: 2
217 <211> LENGTH: 346
218 <212> TYPE: PRT
219 <213> ORGANISM: Bombyx mori
221 <400> SEQUENCE: 2
222 Met Glu Leu Thr Lys Val Ala Lys Asn Gly Ala Ala Ala Thr Leu Val
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RAW SEQUENCE LISTING DATE: 01/27/2002
PATENT APPLICATION: US/10/041,859 TIME: 15:30:42

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223   1               5                  10                  15
225 Met Leu Lys Asn Ala Arg Asp Ala Lys Met Arg Pro Phe Ile Gly Pro
226              20                  25                  30
228 Leu Met Leu Ser Ser Cys Glu Ser Ser Thr Thr Ser Thr Leu Pro Ser
229          35                  40                  45
231 Pro Ser Ser Ser Ala Asp Lys Thr Asp Asn His Asp Thr Phe Asn Phe
232      50                  55                  60
234 Leu Pro Asp Met Pro Asp Met Arg Arg Glu Glu Glu Arg Leu Lys Thr
235  65                  70                  75                  80
237 Phe Asp Gln Trp Pro Val Thr Phe Leu Thr Pro Glu Gln Leu Ala Arg
238                  85                  90                  95
240 Asn Gly Phe Tyr Tyr Leu Gly Arg Gly Asp Glu Val Cys Cys Ala Phe
241              100                 105                 110
243 Cys Lys Val Glu Ile Met Arg Trp Val Glu Gly Asp Asp Pro Ala Ala
244          115                 120                 125
246 Asp His Arg Arg Trp Ala Pro Gln Cys Pro Phe Val Arg Lys Gln Met
247      130                 135                 140
249 Tyr Ala Asn Ala Gly Gly Glu Ala Thr Ala Val Gly Arg Asp Glu Cys
250 145                 150                 155                 160
252 Gly Ala Ser Ala Ala Thr Gln Pro Pro Arg Met Pro Gly Pro Val His
253                 165                 170                 175
255 Ala Arg Tyr Ser Thr Glu Ala Ala Arg Leu Ala Thr Phe Lys Asp Trp
256              180                 185                 190
258 Pro Arg Arg Met Arg Gln Lys Pro Glu Glu Leu Ala Glu Ala Gly Phe
259          195                 200                 205
261 Phe Tyr Thr Gly Gln Gly Asp Lys Thr Lys Cys Phe Tyr Cys Asp Gly
262      210                 215                 220
264 Gly Leu Lys Asp Trp Glu Ser Asp Asp Val Pro Trp Glu Gln His Ala
265 225                 230                 235                 240
267 Arg Trp Phe Asp Arg Cys Ala Tyr Val Gln Leu Val Lys Gly Arg Asp
268                 245                 250                 255
270 Tyr Ile Gln Lys Val Lys Ser Glu Ala Thr Ala Ile Ser Ala Ser Glu
271              260                 265                 270
273 Glu Glu Gln Ala Ala Thr Asn Asp Ser Thr Lys Asn Val Ala Gln Glu
274          275                 280                 285
276 Gly Glu Lys His Leu Asp Asp Ser Lys Ile Cys Lys Ile Cys Tyr Ser
277      290                 295                 300
279 Glu Glu Arg Asn Val Cys Phe Val Pro Cys Gly His Val Val Ala Cys
280 305                 310                 315                 320
282 Ala Lys Cys Ala Leu Ser Thr Asp Lys Cys Pro Met Cys Arg Arg Thr
283                 325                 330                 335
285 Phe Thr Asn Ala Val Arg Leu Tyr Phe Ser
286              340                 345
289 <210> SEQ ID NO: 3
290 <211> LENGTH: 20
291 <212> TYPE: DNA
292 <213> ORGANISM: Artificial Sequence
294 <220> FEATURE:
295 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
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RAW SEQUENCE LISTING DATE: 01/27/2002
PATENT APPLICATION: US/10/041,859 TIME: 15:30:42

Input Set : A:\087102us.app
Output Set: N:\CRF3\01272002\J041859.raw

297 <220> FEATURE:
298 <221> NAME/KEY: modified_base
299 <222> LOCATION: (3)
300 <223> OTHER INFORMATION: a, c, g or t
302 <220> FEATURE:
303 <221> NAME/KEY: modified_base
304 <222> LOCATION: (6)
305 <223> OTHER INFORMATION: a, c, g or t
307 <220> FEATURE:
308 <221> NAME/KEY: modified_base
309 <222> LOCATION: (9)
310 <223> OTHER INFORMATION: a, c, g or t
312 <220> FEATURE:
313 <221> NAME/KEY: modified_base
314 <222> LOCATION: (12)
315 <223> OTHER INFORMATION: a, c, g or t
317 <400> SEQUENCE: 3
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321 <210> SEQ ID NO: 4
322 <211> LENGTH: 17
323 <212> TYPE: DNA
324 <213> ORGANISM: Artificial Sequence
326 <220> FEATURE:
327 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
329 <220> FEATURE:
330 <221> NAME/KEY: modified_base
331 <222> LOCATION: (3)
332 <223> OTHER INFORMATION: a, c, g or t
334 <220> FEATURE:
335 <221> NAME/KEY: modified_base
336 <222> LOCATION: (9)
337 <223> OTHER INFORMATION: a, c, g or t
339 <220> FEATURE:
340 <221> NAME/KEY: modified_base
341 <222> LOCATION: (15)
342 <223> OTHER INFORMATION: a, c, g or t
344 <400> SEQUENCE: 4
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348 <210> SEQ ID NO: 5
349 <211> LENGTH: 18
350 <212> TYPE: DNA
351 <213> ORGANISM: Artificial Sequence
353 <220> FEATURE:
354 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
356 <400> SEQUENCE: 5
357 ctgttcccac ggaacgtc 18
360 <210> SEQ ID NO: 6
361 <211> LENGTH: 17
362 <212> TYPE: DNA

Use of n and/or Xaa has been detected in the Sequence Listing. Review the Sequence Listing to insure a corresponding explanation is presented in the <220> to <223> fields of each sequence using n or Xaa.

VERIFICATION SUMMARY DATE: 01/27/2002
PATENT APPLICATION: US/10/041,859 TIME: 15:30:43

Input Set : A:\087102us.app
Output Set: N:\CRF3\01272002\J041859.raw

L:13 M:270 C: Current Application Number differs, Replaced Application Number
L:14 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:318 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:3
L:345 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:4
L:402 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7
L:405 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:7